

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/874,460

1812

DATE: 12/04/97  
TIME: 15:39:07

INPUT SET: S21923.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

#5 / AR.  
02/04/98

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANTS: WEI, YING-FEI  
KREIDER, BRENT  
ROSEN, CRAIG

(ii) TITLE OF INVENTION: CHEMOKINE BETA 15

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
(B) STREET: 1100 NEW YORK AVENUE, SUITE 600  
(C) CITY: WASHINGTON  
(D) STATE: D.C.  
(E) COUNTRY: US  
(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: (To Be Assigned)  
(B) FILING DATE: HERewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/019,837  
(B) FILING DATE: 17-JUN-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Steffe, Eric K.  
(B) REGISTRATION NUMBER: 36,688  
(C) REFERENCE/DOCKET NUMBER: 1488.0420001

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-371-2600  
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

ENTERED

# RAW SEQUENCE LISTING

## PATENT APPLICATION US/08/874,460

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TIME: 15:39:10

INPUT SET: S21923.raw

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47      (i) SEQUENCE CHARACTERISTICS:
48          (A) LENGTH: 989 base pairs
49          (B) TYPE: nucleic acid
50          (C) STRANDEDNESS: single
51          (D) TOPOLOGY: linear
52
53      (ii) MOLECULE TYPE: DNA (genomic)
54
55
56      (ix) FEATURE:
57          (A) NAME/KEY: CDS
58          (B) LOCATION: 88..534
59
60      (ix) FEATURE:
61          (A) NAME/KEY: sig_peptide
62          (B) LOCATION: 88..147
63
64      (ix) FEATURE:
65          (A) NAME/KEY: mat_peptide
66          (B) LOCATION: 148..534
67
68
69      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
70
71      CCGGCGGGCA TCAGCTCCCT TGACCCAGTG GATATCGGTG GCCCGTTAT TCGTCCAGGT      60
72
73      GCCCAGGGAG GAGGACCCGC CTGCAGC ATG AAC CTG TGG CTC CTG GCC TGC      111
74          Met Asn Leu Trp Leu Leu Ala Cys
75          -20                      -15
76
77      CTG GTG GCC GGC TTC CTG GGA GCC TGG GCC CCC GCT GTC CAC ACC CAA      159
78      Leu Val Ala Gly Phe Leu Gly Ala Trp Ala Pro Ala Val His Thr Gln
79          -10                      -5                      1
80
81      GGT GTC TTT GAG GAC TGC TGC CTG GCC TAC CAC TAC CCC ATT GGG TGG      207
82      Gly Val Phe Glu Asp Cys Cys Leu Ala Tyr His Tyr Pro Ile Gly Trp
83          5                      10                      15                      20
84
85      GCT GTG CTC CGG CGC GCC TGG ACT TAC CGG ATC CAG GAG GTG AGC GGG      255
86      Ala Val Leu Arg Arg Ala Trp Thr Tyr Arg Ile Gln Glu Val Ser Gly
87          25                      30                      35
88
89      AGC TGC AAT CTG CCT GCT GCG ATA TTC TAC CTC CCC AAG AGA CAC AGG      303
90      Ser Cys Asn Leu Pro Ala Ala Ile Phe Tyr Leu Pro Lys Arg His Arg
91          40                      45                      50
92
93      AAG GTG TGT GGG AAC CCC AAA AGC AGG GAG GTG CAG AGA GCC ATG AAG      351
94      Lys Val Cys Gly Asn Pro Lys Ser Arg Glu Val Gln Arg Ala Met Lys
95          55                      60                      65
96
97      CTC CTG GAT GCT CGA AAT AAG GTT TTT GCA AAG CTC CAC CAC AAC ACG      399
98      Leu Leu Asp Ala Arg Asn Lys Val Phe Ala Lys Leu His His Asn Thr
99          70                      75                      80

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100
101 CAG ACC TTC CAA GGC CCT CAT GCT GTA AAG AAG TTG AGT TCT GGA AAC      447
102 Gln Thr Phe Gln Gly Pro His Ala Val Lys Lys Leu Ser Ser Gly Asn
103 85                      90                      95                      100
104
105 TCC AAG TTA TCA TCG TCC AAG TTT AGC AAT CCC ATC AGC AGC AGC AAG      495
106 Ser Lys Leu Ser Ser Ser Lys Phe Ser Asn Pro Ile Ser Ser Ser Lys
107                      105                      110                      115
108
109 AGG AAT GTC TCC CTC CTG ATA TCA GCT AAT TCA GGA CTG TGAGCCGGCT      544
110 Arg Asn Val Ser Leu Leu Ile Ser Ala Asn Ser Gly Leu
111                      120                      125
112
113 CATTTCTGGG CTCCATCGGC ACAGGAGGGC CGGATCTTTC TCCGATAAAA CCGTCGCCCT      604
114
115 ACAGACCCAG CTGTCCCCAC GCCTCTGTCT TTTGGGTCAA GTCTTAATCC CTGCACCTGA      664
116
117 GTTGGTCCTC CCTCTGCACC CCCACCACCT CCTGCCCGTC TGGCAACTGG AAAGAGGGAG      724
118
119 TTGGCCTGAT TTTAAGCCTT TTGCCGCTCC GGGGACCAGC AGCAATCCTG GGCAGCCAGT      784
120
121 GGCTCTTGTA GAGAAGACTT AGGATACCTC TCTCACTTTC TGTTTCTTGC CGTCCACCCC      844
122
123 GGGCCATGCC AGTGTGTCCC TCTGGGTCCC TCCAAAACTC TGGTCAGTTC AAGGATGCCC      904
124
125 CTCCCAGGCT ATGCTTTTCT ATAACCTTTA AATAAACCTT GGGGGGTGAT GGAGTCAAAA      964
126
127 AAAAAAAAAA AAAAAAAAAA AAAAA                      989
128
129
130 (2) INFORMATION FOR SEQ ID NO:2:
131
132 (i) SEQUENCE CHARACTERISTICS:
133 (A) LENGTH: 149 amino acids
134 (B) TYPE: amino acid
135 (D) TOPOLOGY: linear
136
137 (ii) MOLECULE TYPE: protein
138
139 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
140
141 Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
142 -20                      -15                      -10                      -5
143
144 Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
145                      1                      5                      10
146
147 Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr
148                      15                      20                      25
149
150 Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile
151                      30                      35                      40
152

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153 Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser
154 45 50 55 60
155
156
157 Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val
158 65 70 75
159
160 Phe Ala Lys Leu His His Asn Thr Gln Thr Phe Gln Gly Pro His Ala
161 80 85 90
162
163 Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys Phe
164 95 100 105
165
166 Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile Ser
167 110 115 120
168
169 Ala Asn Ser Gly Leu
170 125
171

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(2) INFORMATION FOR SEQ ID NO:3:

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174 (i) SEQUENCE CHARACTERISTICS:
175 (A) LENGTH: 95 amino acids
176 (B) TYPE: amino acid
177 (C) STRANDEDNESS: single
178 (D) TOPOLOGY: linear
179

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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186
187 Ala Thr Glu Thr Lys Glu Val Gln Ser Ser Leu Lys Ala Gln Gln Gly
188 1 5 10 15
189
190 Leu Glu Ile Glu Met Phe His Met Gly Phe Gln Asp Ser Ser Asp Cys
191 20 25 30
192
193 Cys Leu Ser Tyr Asn Ser Arg Ile Gln Cys Ser Arg Phe Ile Gly Tyr
194 35 40 45
195
196 Phe Pro Ile Ser Gly Gly Cys Thr Arg Pro Gly Ile Ile Phe Ile Ser
197 50 55 60
198
199 Lys Arg Gly Phe Gln Val Cys Ala Asn Pro Ser Asp Arg Arg Val Gln
200 65 70 75 80
201
202 Arg Cys Arg Leu Glu Gln Asn Ser Gln Pro Arg Thr Tyr Lys Gln
203 85 90 95
204

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(2) INFORMATION FOR SEQ ID NO:4:

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PATENT APPLICATION US/08/874,460DATE: 12/04/97  
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206  
207 (i) SEQUENCE CHARACTERISTICS:  
208 (A) LENGTH: 27 base pairs  
209 (B) TYPE: nucleic acid  
210 (C) STRANDEDNESS: single  
211 (D) TOPOLOGY: linear  
212  
213 (ii) MOLECULE TYPE: DNA (genomic)  
214  
215  
216  
217  
218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
219  
220 GCCGTCGACG TCCACACCCA AGGTGTC 27  
221  
222 (2) INFORMATION FOR SEQ ID NO:5:  
223  
224 (i) SEQUENCE CHARACTERISTICS:  
225 (A) LENGTH: 30 base pairs  
226 (B) TYPE: nucleic acid  
227 (C) STRANDEDNESS: single  
228 (D) TOPOLOGY: linear  
229  
230 (ii) MOLECULE TYPE: DNA (genomic)  
231  
232  
233  
234  
235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
236  
237 GCCTCTAGAG GAGCCCAGAA ATGAGCCGGC 30  
238  
239 (2) INFORMATION FOR SEQ ID NO:6:  
240  
241 (i) SEQUENCE CHARACTERISTICS:  
242 (A) LENGTH: 36 base pairs  
243 (B) TYPE: nucleic acid  
244 (C) STRANDEDNESS: single  
245 (D) TOPOLOGY: linear  
246  
247 (ii) MOLECULE TYPE: DNA (genomic)  
248  
249  
250  
251  
252 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
253  
254 GCCTCTAGAG CCATCATGAA CCTGTGGCTC CTGGCC 36  
255  
256 (2) INFORMATION FOR SEQ ID NO:7:  
257  
258 (i) SEQUENCE CHARACTERISTICS:

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/874,460**

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*INPUT SET: S21923.raw*

Line	Error	Original Text
28	Wrong application Serial Number	(A) APPLICATION NUMBER: (To Be Assigned)